



results of BLAST

BLASTN 2.2.8 [Jan-05-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1078329956-32040-6999318735.BLASTQ3

Query=

(18 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

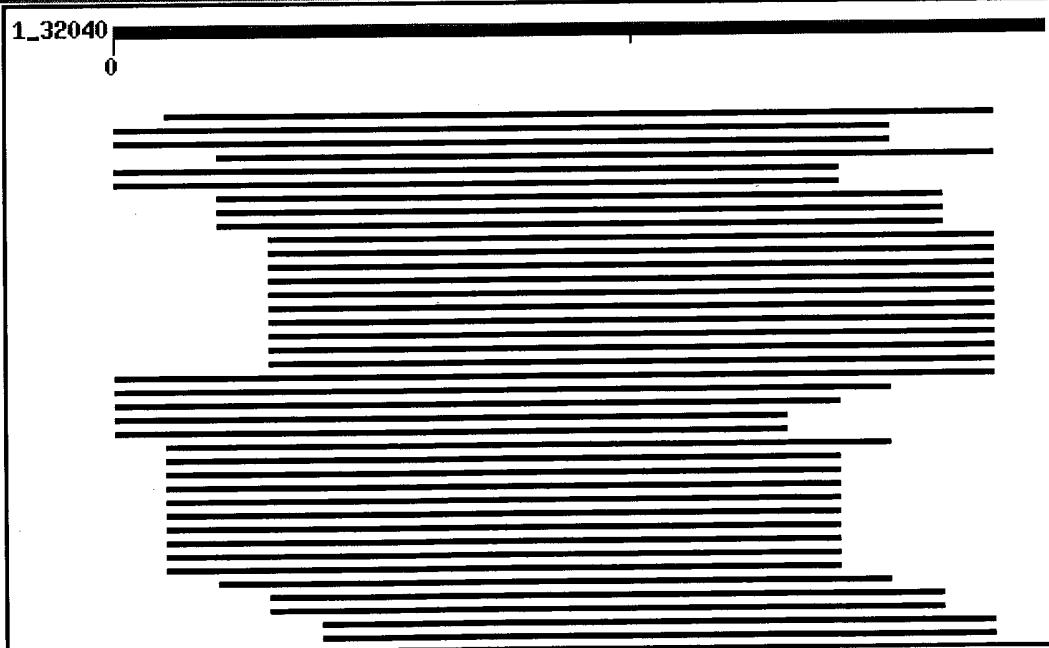
2,092,142 sequences; 10,066,846,959 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 126 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score (bits)	E Value
-----------------	------------

complete sequence
Length = 204385

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 4 gatgcgtttagcatc 18
||||| ||||| |||||
Sbjct: 13201 gatgcgtttagcatc 13215

>gi|14701993|gb|AC092492.1|AC092492 Drosophila melanogaster, chromosome 2L,
BACR20B09, complete sequence
Length = 177997

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 3 cgatgcgtttagcat 17
||||| ||||| |||||
Sbjct: 34878 cgatgcgtttagcat 34892

>gi|31559209|emb|AL954382.2| Mouse DNA sequence from clone RP23-214G6 on chrom
sequence
Length = 185335

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 4 gatgcgtttagcatc 18
||||| ||||| |||||
Sbjct: 139235 gatgcgtttagcatc 139249

>gi|4732009|gb|AF118538.1|AF118538 Erigeron vagus internal transcribed spacer 1,
gene, and internal transcribed spacer 2, complete
sequence
Length = 625

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 4 gatgcgtttagcatc 18
||||| ||||| |||||
Sbjct: 54 gatgcgtttagcatc 68

>gi|4731993|gb|AF118522.1|AF118522 Erigeron bellidioides internal transcribed spacer
RNA gene, and internal transcribed spacer 2, complete
sequence
Length = 625

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 4 gatgcgtttagcatc 18
||||| ||||| |||||

□ >gi|38257244|gb|AC123835.4| Mus musculus BAC clone RP23-365J20 from chromosome
Length = 219799

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 4 gatgcgtttagcatc 18
|||||||
Sbjct: 98656 gatgcgtttagcatc 98670

□ >gi|31296414|gb|AF511588.1| Erigeron bellidioides internal transcribed spacer 1, 5'
RNA gene, and internal transcribed spacer 2, complete
sequence
Length = 678

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 4 gatgcgtttagcatc 18
|||||||
Sbjct: 54 gatgcgtttagcatc 68

□ >gi|3218114|emb|Z99288.1|CEZK262| Caenorhabditis elegans cosmid ZK262, complete
Length = 39555

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 4 gatgcgtttagcatc 18
|||||||
Sbjct: 13572 gatgcgtttagcatc 13586

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Minus

Query: 4 gatgcgtttagcatc 18
|||||||
Sbjct: 10212 gatgcgtttagcatc 10198

□ >gi|22946015|gb|AE003624.2| Drosophila melanogaster chromosome 2L section 3:
sequence
Length = 270775

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 3 cgatgcgtttagcat 17
|||||||
Sbjct: 88657 cgatgcgtttagcat 88671

□ >gi|38044060|emb|BX004783.13| Zebrafish DNA sequence from clone DKEY-14E1 in]

Sbjct: 54 gatgcgttggcatc 68

 □>gi|13897862|gb|AF259295.1|AF259295 Taxus brevifolia specimen-voucher 1087-88A
 spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and 26S
 ribosomal RNA gene, partial sequence
 Length = 1131

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Minus

Query: 1 accgatgcgttggac 15

 |||||||||||||||

Sbjct: 685 accgatgcgttggac 671

 □>gi|3810578|gb|AC005889.1|AC005889 Drosophila melanogaster, chromosome 2L, 1
 DS06958 and DS03097, complete sequence
 Length = 108924

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Plus

Query: 3 cgatgcgttggcat 17

 |||||||||||||||

Sbjct: 84509 cgatgcgttggcat 84523

 □>gi|41056569|gb|AY422089.1| Astatotilapia burtoni estrogen receptor alpha mRNA,
 Length = 4037

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Minus

Query: 4 gatgcgttggcatc 18

 |||||||||||||||

Sbjct: 1564 gatgcgttggcatc 1550

 □>gi|11095052|gb|AC084602.1|CBRG43K20 Caenorhabditis briggsae cosmid G43K20, cc
 Length = 43998

Score = 30.2 bits (15), Expect = 8.0
Identities = 15/15 (100%)
Strand = Plus / Minus

Query: 1 accgatgcgttggac 15

 |||||||||||||||

Sbjct: 19336 accgatgcgttggac 19322

 □>gi|39656039|gb|AY320035.1| Bacteriophage VWB, complete genome
 Length = 49220

Score = 28.2 bits (14), Expect = 32
Identities = 14/14 (100%)
Strand = Plus / Minus

Query: 2 ccgatgcgttggac 15

|||||||
Sbjct: 32804 ccgatgcgttggc 32791

[>]gi|21723490|gb|AY078159.2| Delftia acidovorans insertion sequence IS1071 trar
cds; insertion sequence IS1380 transposase, hypothetical
protein, LysR-type transcriptional regulator (tfdR),
chlorocatechol 1,2-dioxygenase (tfdC), chloromuconate
cycloisomerase (tfdD), hypothetical protein,
chlorodienlactone hydrolase (tfdE), chloromaleylacetate
reductase (tfdF), hypothetical protein, hypothetical
protein, 2,4-D/alpha-ketoglutarate dioxygenase (tfdA),
putative transport protein (tfdK), dichlorophenol
hydroxylase (tf>
Length = 28423

Score = 28.2 bits (14), Expect = 32
Identities = 14/14 (100%)
Strand = Plus / Minus

Query: 2 ccgatgcgttggc 15
|||||||
Sbjct: 25604 ccgatgcgttggc 25591

Score = 28.2 bits (14), Expect = 32
Identities = 14/14 (100%)
Strand = Plus / Plus

Query: 2 ccgatgcgttggc 15
|||||||
Sbjct: 1383 ccgatgcgttggc 1396

[>]gi|28573983|ref|NM_175942.1| Drosophila melanogaster CG33127-PA [Drosophilae]
(CG33127) mRNA, complete cds
Length = 855

Score = 28.2 bits (14), Expect = 32
Identities = 14/14 (100%)
Strand = Plus / Minus

Query: 1 accgatgcgttgg 14
|||||||
Sbjct: 382 accgatgcgttgg 369

[>]gi|28855325|gb|AE016874.1| Pseudomonas syringae pv. tomato str. DC3000 section
complete genome
Length = 310029

Score = 28.2 bits (14), Expect = 32
Identities = 14/14 (100%)
Strand = Plus / Plus

Query: 1 accgatgcgttgg 14
|||||||
Sbjct: 171160 accgatgcgttgg 171173

Score = 24.3 bits (12), Expect = 492
Identities = 12/12 (100%)
Strand = Plus / Minus



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RID: 1078328153-5223-206890238348.BLASTQ3

Query=

(42 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

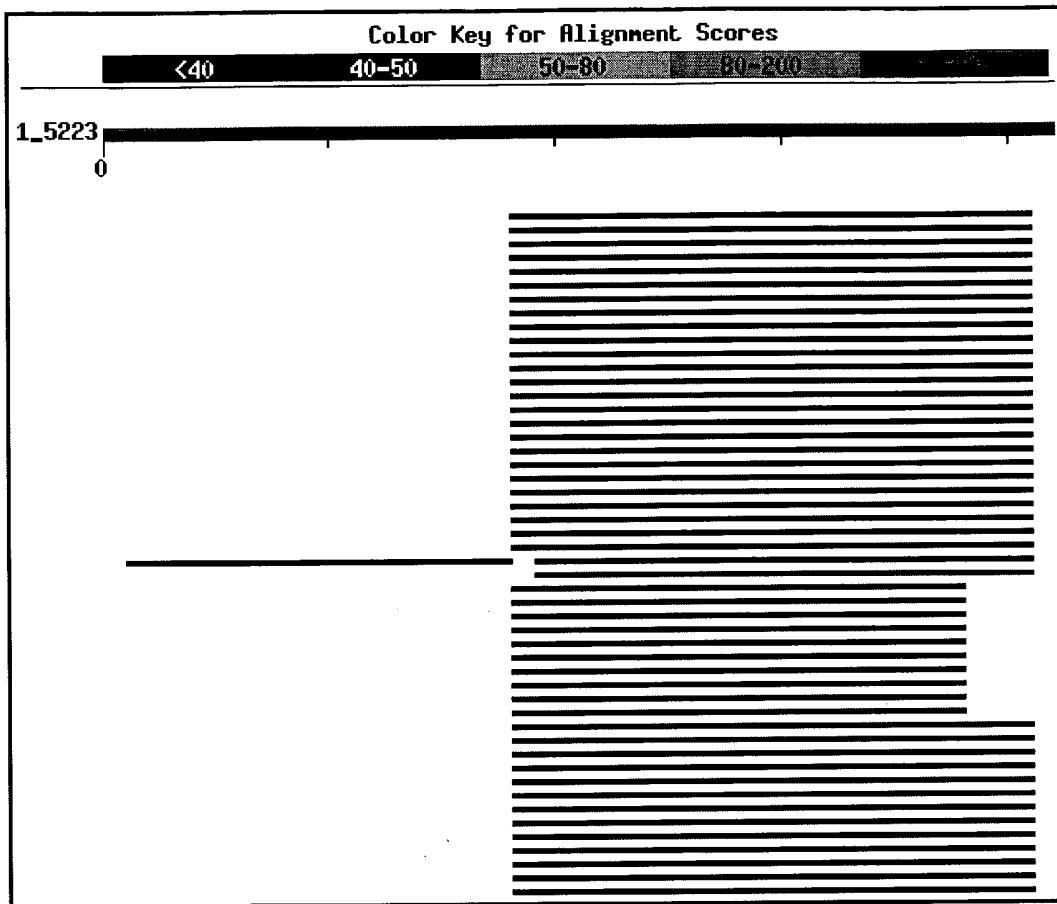
2,092,142 sequences; 10,066,846,959 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 62 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

		Score (bits)	E Value	
gi 40226235 gb BC014085.2	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L
gi 40226183 gb BC023632.2	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L
gi 19684109 gb BC025925.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 14290602 gb BC009081.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 33871196 gb BC004109.2	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 38196986 gb BC013310.2	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L
gi 20070829 gb BC026907.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 12804398 gb BC001601.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 20809305 gb BC029618.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 30584592 gb BT007877.1	Synthetic construct Homo sapiens...	48	7e-04	
gi 30582624 gb BT006893.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 10439402 dbj AK026525.1	Homo sapiens cDNA: FLJ22872 fis...	48	7e-04	L U G
gi 17946825 gb BC020308.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 20379463 gb BC029340.1	Homo sapiens glyceraldehyde-3-ph...	48	7e-04	L U
gi 31644 emb X01677.1 HSGAPDR	Human liver mRNA for glyceral...	48	7e-04	L U G
gi 16444668 emb AL139811.30	Human DNA sequence from clone ...	48	7e-04	
gi 35052 emb X53778.1 HSNGMRNA	H.sapiens hng mRNA for uraci...	48	7e-04	L G
gi 9802301 gb AF261085.1 AF261085	Homo sapiens glyceraldehy...	48	7e-04	L
gi 182860 gb M17851.1 HUMG3PDB	Human glyceraldehyde-3-phosp...	48	7e-04	L G

gi 9956034 gb AY007133.1	Homo sapiens clone CDABP0047 mRNA...	48	7e-04	L	G
gi 182976 gb M33197.1 HUMGAPDH	Human glyceraldehyde-3-phosp...	48	7e-04	L	
gi 182862 gb J02642.1 HUMG3PDC	Human glyceraldehyde 3-phosp...	48	7e-04	L	
gi 6983846 dbj AB038240.1	Canis familiaris GAPDH mRNA for ...	48	7e-04	G	
gi 21104391 dbj AB062273.1	Homo sapiens OK/SW-cl.12 mRNA f...	48	7e-04	L	
gi 7669491 ref NM_002046.2	Homo sapiens glyceraldehyde-3-p...	48	7e-04	L	G
gi 3859551 gb AF097177.1 AF097177	Felis catus glyceraldehyd...	46	0.003		
gi 9652124 gb AF272837.1 AF272837	Ovis aries glyceraldehyde...	46	0.003		
gi 32891804 gb AY340484.1	Homo sapiens glyceraldehyde-3-ph...	42	0.046		
gi 28191361 gb AC006064.10	Homo sapiens 12 PAC RP5-940J5 (...	42	0.046	L G	
gi 15883201 emb AJ338783.1 HSA338783	Homo sapiens genomic s...	42	0.046		
gi 15886028 emb AJ341610.1 HSA341610	Homo sapiens genomic s...	42	0.046		
gi 15885949 emb AJ341531.1 HSA341531	Homo sapiens genomic s...	42	0.046		
gi 15885635 emb AJ341217.1 HSA341217	Homo sapiens genomic s...	42	0.046		
gi 15884975 emb AJ340557.1 HSA340557	Homo sapiens genomic s...	42	0.046		
gi 15885622 emb AJ341204.1 HSA341204	Homo sapiens genomic s...	42	0.046		
gi 15869769 emb AJ325375.1 HSA325375	Homo sapiens genomic s...	42	0.046		
gi 182980 gb J04038.1 HUMGAPDHG	Human glyceraldehyde-3-phos...	42	0.046	L	
gi 34881158 ref XM_343809.1	Rattus norvegicus similar to g...	40	0.18	L	
gi 2407183 gb AF017079.1	Sus scrofa glyceraldehyde 3-phosp...	40	0.18		
gi 41634588 emb BX934060.1	Gallus gallus finished cDNA, cl...	40	0.18		
gi 28209423 gb AC091810.3	Homo sapiens chromosome X clone ...	40	0.18		
gi 63402 emb V00407.1 GGGAPD	Gallus gallus mRNA encoding gl...	40	0.18	L	
gi 62615 emb Z19086.1 CCGLYDEHA	C.coturnix encoding glycera...	40	0.18		
gi 16930717 gb AF439784.1 AF439784	Sus scrofa glyceraldehyd...	40	0.18		
gi 32993853 dbj AK108644.1	Oryza sativa (japonica cultivar...	40	0.18		
gi 4105595 gb AF047874.1 AF047874	Gallus gallus glyceraldehy...	40	0.18	L	
gi 28189720 dbj AB098985.1	Bos taurus mRNA for similar to ...	40	0.18		
gi 28189708 dbj AB098979.1	Bos taurus mRNA for similar to ...	40	0.18		
gi 28189618 dbj AB098934.1	Bos taurus mRNA for similar to ...	40	0.18		
gi 28189564 dbj AB098907.1	Bos taurus mRNA for similar to ...	40	0.18		
gi 2687660 gb AF036934.1 AF036934	Columba livia glyceraldeh...	40	0.18		
gi 31643 emb X01111.1 HSGAPDP	Human x-linked GAPD pseudogen...	40	0.18	L	
gi 406106 gb L23961.1 RABGLY3PHO	Oryctolagus cuniculus glyc...	40	0.18		
gi 211800 gb K01458.1 CHKGAPDHA	Chicken GAPDH (glyceraldehy...	40	0.18	L	
gi 204248 gb M17701.1 RATGAPDHA	Rat glyceraldehyde-3-phosph...	40	0.18	L	G
gi 38174575 gb BC060964.1	Mus musculus cDNA clone MGC:7405...	36	2.8		
gi 21645928 gb AE012784.1	Chlorobium tepidum TLS section ...	36	2.8		
gi 12859062 dbj AK019052.1	Mus musculus adult male stomach...	36	2.8	L	
gi 12836361 dbj AK004859.1	Mus musculus adult male liver c...	36	2.8	L	
gi 26324519 dbj AK028573.1	Mus musculus 10 days neonate sk...	36	2.8	L	
gi 22137419 gb BC029194.1	Mus musculus cDNA clone IMAGE:44...	36	2.8	L	
gi 27369482 ref NM_172395.1	Mus musculus small protein eff...	36	2.8	L	

Alignments

 Get selected sequences Select all Deselect all

>gi|40226235|gb|BC014085.2| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase clone MGC:20338 IMAGE:4541305), complete cds Length = 2096

Score = 48.1 bits (24), Expect = 7e-04

Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggctggagtcacggatt 42
|||||||
Sbjct: 879 ggtgaaggctggagtcacggatt 902

>gi|40226183|gb|BC023632.2| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (clone MGC:23503 IMAGE:4842418), complete cds
Length = 1307

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggctggagtcacggatt 42
|||||||
Sbjct: 33 ggtgaaggctggagtcacggatt 56

>gi|19684109|gb|BC025925.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (clone MGC:15497 IMAGE:2989348), complete cds
Length = 1312

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggctggagtcacggatt 42
|||||||
Sbjct: 66 ggtgaaggctggagtcacggatt 89

>gi|14290602|gb|BC009081.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (clone MGC:9901 IMAGE:3869809), complete cds
Length = 1288

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggctggagtcacggatt 42
|||||||
Sbjct: 70 ggtgaaggctggagtcacggatt 93

>gi|33871196|gb|BC004109.2| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (clone MGC:11042 IMAGE:3678259), complete cds
Length = 1287

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggctggagtcacggatt 42
|||||||
Sbjct: 61 ggtgaaggctggagtcacggatt 84

>gi|38196986|gb|BC013310.2| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (clone MGC:4765 IMAGE:3538383), complete cds
Length = 1303

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggatcaacggatt 42
|||||||
Sbjct: 69 ggtgaaggtcgaggatcaacggatt 92

>gi|20070829|gb|BC026907.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
clone MGC:25010 IMAGE:4454083), complete cds
Length = 1261

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggatcaacggatt 42
|||||||
Sbjct: 47 ggtgaaggtcgaggatcaacggatt 70

>gi|12804398|gb|BC001601.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
clone MGC:2031 IMAGE:3543589), complete cds
Length = 1286

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggatcaacggatt 42
|||||||
Sbjct: 63 ggtgaaggtcgaggatcaacggatt 86

>gi|20809305|gb|BC029618.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
clone MGC:9949 IMAGE:3876535), complete cds
Length = 1301

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggatcaacggatt 42
|||||||
Sbjct: 63 ggtgaaggtcgaggatcaacggatt 86

>gi|30584592|gb|BT007877.1| Synthetic construct Homo sapiens glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
Length = 1008

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggatcaacggatt 42
|||||||
Sbjct: 9 ggtgaaggtcgaggatcaacggatt 32

>gi|30582624|gb|BT006893.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
Length = 1008

complete cds
Length = 1008

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggactaacggatt 42
|||||||
Sbjct: 9 ggtgaaggtcgaggactaacggatt 32

>gi|10439402|dbj|AK026525.1| Homo sapiens cDNA: FLJ22872 fis, clone KAT025
HUMGAPDH Human glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) mRNA
Length = 1228

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggactaacggatt 42
|||||||
Sbjct: 134 ggtgaaggtcgaggactaacggatt 157

>gi|17946825|gb|BC020308.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase
clone IMAGE:4938218)
Length = 1263

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggactaacggatt 42
|||||||
Sbjct: 47 ggtgaaggtcgaggactaacggatt 70

>gi|20379463|gb|BC029340.1| Homo sapiens glyceraldehyde-3-phosphate dehydrogenase
clone IMAGE:3917859)
Length = 1272

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggactaacggatt 42
|||||||
Sbjct: 55 ggtgaaggtcgaggactaacggatt 78

>gi|31644|emb|X01677.1|HSGAPDR Human liver mRNA for glyceraldehyde-3-phosphate dehydrogenase
(G3PD, EC 1.2.1.12)
Length = 1272

Score = 48.1 bits (24), Expect = 7e-04
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 19 ggtgaaggtcgaggactaacggatt 42
|||||||
Sbjct: 69 ggtgaaggtcgaggactaacggatt 92